1633

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: FLECKENSTEIN, Bernhard
ALBRECHT, Jens-Christian
NEIPEL, Frank
FRIEDMAN-KIEN, Alvin
HUANG, Yao-Qi

(ii) TITLE OF INVENTION: VIRAL INTERLEUKIN-6

(iii) NUMBER OF SEQUENCES: 4

(iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: FOLEY & LARDNER
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(D) STATE: D.C.
(E) COUNTRY: U.S.A.
(F) ZIP: 20007-5109

(v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: US 09/230,048
(B) FILING DATE: 12-MAR-1999
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: WO PCT/EP96/03199
(B) FILING DATE: 19-JUL-1996

(viii) ATTORNEY/AGENT INFORMATION:
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(ix) TELECOMMUNICATION INFORMATION:
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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 612 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..612

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

```
ATG TGC TGG TTC AAG TTG TGG TCT CTC TTG CTG GTC GGT TCA CTG CTG          48
Met Cys Trp Phe Lys Leu Trp Ser Leu Leu Leu Val Gly Ser Leu Leu
 1               5                  10                  15

GTA TCT GGA ACG CGG GGC AAG TTG CCG GAC GCC CCC GAG TTT GAA AAG          96
Val Ser Gly Thr Arg Gly Lys Leu Pro Asp Ala Pro Glu Phe Glu Lys
            20                  25                  30

GAT CTT CTC ATT CAG AGA CTC AAT TGG ATG CTA TGG GTG ATC GAT GAA         144
Asp Leu Leu Ile Gln Arg Leu Asn Trp Met Leu Trp Val Ile Asp Glu
        35                  40                  45

TGC TTC CGC GAC CTC TGT TAC CGT ACC GGC ATC TGC AAG GGT ATT CTA         192
Cys Phe Arg Asp Leu Cys Tyr Arg Thr Gly Ile Cys Lys Gly Ile Leu
    50                  55                  60

GAG CCC GCT GCT ATT TTT CAT CTG AAA CTA CCA GCC ATC AAC GAT ACT         240
Glu Pro Ala Ala Ile Phe His Leu Lys Leu Pro Ala Ile Asn Asp Thr
65                  70                  75                  80

GAT CAC TGC GGG TTA ATA GGA TTT AAT GAG ACT AGC TGC CTT AAA AAG         288
Asp His Cys Gly Leu Ile Gly Phe Asn Glu Thr Ser Cys Leu Lys Lys
                85                  90                  95

CTC GCC GAT GGC TTT TTT GAA TTC GAG GTG TTG TTT AAG TTT TTA ACG         336
Leu Ala Asp Gly Phe Phe Glu Phe Glu Val Leu Phe Lys Phe Leu Thr
            100                 105                 110

ACG GAG TTT GGA AAA TCA GTG ATA AAC GTG GAC GTC ATG GAG CTT CTG         384
Thr Glu Phe Gly Lys Ser Val Ile Asn Val Asp Val Met Glu Leu Leu
        115                 120                 125

ACG AAG ACC TTA GGA TGG GAC ATA CAG GAA GAG CTC AAT AAG CTG ACT         432
Thr Lys Thr Leu Gly Trp Asp Ile Gln Glu Glu Leu Asn Lys Leu Thr
    130                 135                 140

AAG ACG CAC TAC AGT CCA CCC AAA TTT GAC CGC GGT CTA TTA GGG AGG         480
Lys Thr His Tyr Ser Pro Pro Lys Phe Asp Arg Gly Leu Leu Gly Arg
145                 150                 155                 160

CTT CAG GGA CTT AAG TAT TGG GTG AGA CAC TTT GCT TCG TTT TAT GTT         528
Leu Gln Gly Leu Lys Tyr Trp Val Arg His Phe Ala Ser Phe Tyr Val
                165                 170                 175

CTG AGT GCA ATG GAA AAG TTT GCA GGT CAA GCG GTG CGT GTT TTG GAC         576
Leu Ser Ala Met Glu Lys Phe Ala Gly Gln Ala Val Arg Val Leu Asp
            180                 185                 190

TCT ATC CCA GAC GTG ACT CCT GAC GTC CAC GAT AAG                         612
Ser Ile Pro Asp Val Thr Pro Asp Val His Asp Lys
        195                 200
```

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 204 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

```
Met Cys Trp Phe Lys Leu Trp Ser Leu Leu Leu Val Gly Ser Leu Leu
 1               5                  10                  15

Val Ser Gly Thr Arg Gly Lys Leu Pro Asp Ala Pro Glu Phe Glu Lys
            20                  25                  30

Asp Leu Leu Ile Gln Arg Leu Asn Trp Met Leu Trp Val Ile Asp Glu
        35                  40                  45

Cys Phe Arg Asp Leu Cys Tyr Arg Thr Gly Ile Cys Lys Gly Ile Leu
    50                  55                  60

Glu Pro Ala Ala Ile Phe His Leu Lys Leu Pro Ala Ile Asn Asp Thr
65                  70                  75                  80

Asp His Cys Gly Leu Ile Gly Phe Asn Glu Thr Ser Cys Leu Lys Lys
                85                  90                  95

Leu Ala Asp Gly Phe Phe Glu Phe Glu Val Leu Phe Lys Phe Leu Thr
            100                 105                 110

Thr Glu Phe Gly Lys Ser Val Ile Asn Val Asp Val Met Glu Leu Leu
        115                 120                 125

Thr Lys Thr Leu Gly Trp Asp Ile Gln Glu Glu Leu Asn Lys Leu Thr
    130                 135                 140

Lys Thr His Tyr Ser Pro Pro Lys Phe Asp Arg Gly Leu Leu Gly Arg
145                 150                 155                 160

Leu Gln Gly Leu Lys Tyr Trp Val Arg His Phe Ala Ser Phe Tyr Val
                165                 170                 175

Leu Ser Ala Met Glu Lys Phe Ala Gly Gln Ala Val Arg Val Leu Asp
            180                 185                 190

Ser Ile Pro Asp Val Thr Pro Asp Val His Asp Lys
        195                 200
```

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 212 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

```
Met Asn Ser Phe Ser Thr Ser Ala Phe Gly Pro Val Ala Phe Ser Leu
1               5                  10                  15

Gly Leu Leu Leu Val Leu Pro Ala Ala Phe Pro Ala Pro Val Pro Pro
            20                  25                  30

Gly Glu Asp Ser Lys Asp Val Ala Ala Pro His Arg Gln Pro Leu Thr
        35                  40                  45
```

Ser Ser Glu Arg Ile Asp Lys Gln Ile Arg Tyr Ile Leu Asp Gly Ile
50 55 60

Ser Ala Leu Arg Lys Glu Thr Cys Asn Lys Ser Asn Met Cys Glu Ser
65 70 75 80

Ser Lys Glu Ala Leu Ala Glu Asn Asn Leu Asn Leu Pro Lys Met Ala
85 90 95

Glu Lys Asp Gly Cys Phe Gln Ser Gly Phe Asn Glu Glu Thr Cys Leu
100 105 110

Val Lys Ile Ile Thr Gly Leu Leu Glu Phe Glu Val Tyr Leu Glu Tyr
115 120 125

Leu Gln Asn Arg Phe Glu Ser Ser Glu Glu Gln Ala Arg Ala Val Gln
130 135 140

Met Ser Thr Lys Val Leu Ile Gln Phe Leu Gln Lys Lys Ala Lys Asn
145 150 155 160

Leu Asp Ala Ile Thr Thr Pro Asp Pro Thr Thr Asn Ala Ser Leu Leu
165 170 175

Thr Lys Leu Gln Ala Gln Asn Gln Trp Leu Gln Asp Met Thr Thr His
180 185 190

Leu Ile Leu Arg Ser Phe Lys Glu Phe Leu Gln Ser Ser Leu Arg Ala
195 200 205

Leu Arg Gln Met
210

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 211 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Lys Phe Leu Ser Ala Arg Asp Phe His Pro Val Ala Phe Leu Gly
1 5 10 15

Leu Met Leu Val Thr Thr Thr Ala Phe Pro Thr Ser Gln Val Arg Arg
20 25 30

Gly Asp Phe Thr Glu Asp Thr Thr Pro Asn Arg Pro Val Tyr Thr Thr
35 40 45

Ser Gln Val Gly Gly Leu Ile Thr His Val Leu Trp Glu Ile Val Glu
50 55 60

Met Arg Lys Glu Leu Cys Asn Gly Asn Ser Asp Cys Met Asn Asn Asp
65 70 75 80

```
Asp Ala Leu Ala Glu Asn Asn Leu Lys Leu Pro Glu Ile Gln Arg Asn
                 85                  90                  95

Asp Gly Cys Tyr Gln Thr Gly Tyr Asn Gln Glu Ile Cys Leu Leu Lys
            100                 105                 110

Ile Ser Ser Gly Leu Leu Glu Tyr His Ser Tyr Leu Glu Tyr Met Lys
        115                 120                 125

Asn Asn Leu Lys Asp Asn Lys Lys Asp Lys Ala Arg Val Leu Gln Arg
    130                 135                 140

Asp Thr Glu Thr Leu Ile His Ile Phe Asn Gln Glu Val Lys Asp Leu
145                 150                 155                 160

His Lys Ile Val Leu Pro Thr Pro Ile Ser Asn Ala Leu Leu Thr Asp
                165                 170                 175

Lys Leu Glu Ser Gln Lys Glu Trp Leu Arg Thr Lys Thr Ile Gln Phe
            180                 185                 190

Ile Leu Lys Ser Leu Glu Glu Phe Leu Lys Val Thr Leu Arg Ser Thr
        195                 200                 205

Arg Gln Thr
    210
```